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UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/521,571	05/16/2005	James Langham Dale	23558-0017	4029

61263   7590   07/27/2007

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EXAMINER
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ART UNIT	PAPER NUMBER
1638	

MAIL DATE	DELIVERY MODE
07/27/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

	Application No.	Applicant(s)
Office Action Summary	10/521,571	DALE ET AL.
	Examiner	Art Unit	
	Cathy K. Worley	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>1</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>18 January 2005</u>.

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) <u>1 and 70-138</u> is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) _____ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) <u>1 and 70-138</u> are subject to restriction and/or election requirement.
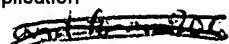
Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All   b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☐ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date _____.

4) ☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____ .

5) ☐ Notice of Informal Patent Application

6) ☒ Other: *sequence alignment.*

DETAILED ACTION

Election/Restrictions

1.   The restriction requirement mailed on July 3, 2007 is VACATED because it was mailed to the incorrect address. The restriction requirement in this office action replaces the previous one, and the time for reply is ONE MONTH from the mail date of this office action.

2.   Restriction is required under 35 U.S.C. 121 and 372.

3.   This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In accordance with 37 CFR 1.499, applicant is required, in reply to this action, to elect a single invention to which the claims must be restricted.

Groups I-IV, claim(s) 1, 70-77, 87-89, 93-108, 78-80 (in part), and 90-92 (in part), drawn to DNA molecules and constructs comprising specified polynucleotides; wherein the specified polynucleotides for groups I-IV are defined by their relationship to SEQ ID NO: 6-9, respectively.

Groups V-VII, claim(s) 81-82, 84, 83 (in part), and 85 (in part), drawn to

polynucleotides comprising nucleotide sequences that encode specified amino acid

sequences; wherein the specified amino acid sequence for groups V-VII is SEQ ID

NO: 3-5, respectively.

Groups VIII-X, claim(s) 86 (in part), drawn to an isolated polypeptide comprising a

specified amino acid sequence; wherein the specified amino acid sequence for groups

VIII-X is SEQ ID NO: 4-6, respectively.

Group XI, claim(s) 109-121, drawn to a method for gene expression in a plant,

comprising introducing an isolated promoter or biologically active fragment thereof

or variant of these.

Group XII, claim(s) 122, drawn to progeny obtained from a differentiated transgenic

plant.

Group XIII, claim(s) 123, drawn to a plant part of a differentiated transgenic plant.

Group XIV, claim(s) 124, drawn to a differentiated transgenic plant regenerated

from transformed plant cells.

Group XV, claim(s) 125-133, drawn to a transformed plant cell and transgenic plant.

Group XVI, claim(s) 134, drawn to a method of using a chimeric DNA construct.

Group XVII, claim(s) 135, drawn to a method for diagnosing a badnaviral infection of a plant.

Groups XVIII-XXVI, claim(s) 137 and 136 (in part), drawn to a method of screening for an agent that modulates badnaviral infection that utilizes either a polypeptide with a specified amino acid sequence or a polynucleotide with a specified nucleic acid sequence; wherein the specified sequence for groups XVIII-XXVI is SEQ ID NO: 1-9, respectively.

Groups XXVII-XXXV, claim(s) 138 (in part), drawn to a method for treating and/or preventing a badnaviral infection of a plant that utilizes either a polypeptide with a specified amino acid sequence or a polynucleotide with a specified nucleic acid sequence; wherein the specified sequence for groups XXVII-XXXV is SEQ ID NO: 1-9, respectively.

4.   The inventions listed as Groups I-XXXV do not relate to a single general

inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the

same or corresponding special technical features for the following reasons:

The technical feature linking groups I-XXXV is an isolated DNA comprising a

promoter upstream of SEQ ID NO:1 or upstream of a sequence that hybridizes to

SEQ ID NO:1 or a fragment or variant; or a coding sequence comprising SEQ ID

NO:1 or a variant or portion thereof; or a polypeptide encoded by SEQ ID NO:1 or a

variant or portion. SEQ ID NO:1 encodes 3 open reading frames (ORFs) from the

Taro bacilliform virus (TaBV) (see first page 4 of the instant specification). Huang

et al teach the genomic sequence of the *Citrus yellow mosaic virus* in their article

"Cloning and sequence analysis of an infectious clone of *Citrus yellow mosaic virus*

that can infect sweet orange via *Agrobacterium*-mediated inoculation" (see J. of

Gen. Virol. (2001) Vol. 82, pp. 2549-2558). They teach that the genomes of all

badnaviruses have similar genome organization and contain three open reading

frames capable of encoding proteins with a molecule mass greater than 10 kDa (see

paragraph bridging pages 2549-2550). The amino acid sequence of one of the

proteins encoded by the virus taught by Huang et al is published in GenBank

Accession NP_569153 (See Huang et al (2001) GenBank accession NP_569153.1).

This protein shares substantial homology with the protein encoded by the instant

SEQ ID NO:1 (see alignment). This demonstrates that the genomic sequence

taught by Huang et al encodes a "portion" and a "variant" of the proteins encoded by

the instant SEQ ID NO:1. Therefore, the technical feature linking the inventions of

groups I-XXXV does not constitute a special technical feature as defined by PCT

Rule 13.2 as it does not define a contribution over the prior art.

Accordingly, Groups I-XXXV are not so linked by the same or a corresponding

special technical feature as to form a single general inventive concept.

5.   Applicant is advised that the reply to this requirement to be complete must

include (i) an election of a species or invention to be examined even though the

requirement be traversed (37 CFR 1.143) and (ii) identification of the claims

encompassing the elected invention.

The election of an invention or species may be made with or without traverse.

To reserve a right to petition, the election must be made with traverse. If the reply

does not distinctly and specifically point out supposed errors in the restriction

requirement, the election shall be treated as an election without traverse.

Should applicant traverse on the ground that the inventions or species are

not patentably distinct, applicant should submit evidence or identify such evidence

now of record showing the inventions or species to be obvious variants or clearly

admit on the record that this is the case. In either instance, if the examiner finds

one of the inventions unpatentable over the prior art, the evidence or admission

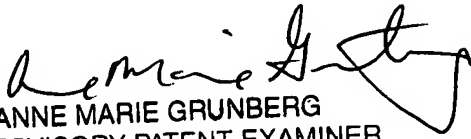may be used in a rejection under 35 U.S.C.103(a) of the other invention.

6.   Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

7.   Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cathy K. Worley whose telephone number is (571) 272-8784. The examiner has a variable schedule but can normally be reached on M-F 10:00 - 4:00 with additional variable hours before 10:00 and after 4:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on (571) 272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the

Patent Application Information Retrieval (PAIR) system. Status information for

published applications may be obtained from either Private PAIR or Public PAIR.

Status information for unpublished applications is available through Private PAIR

only. For more information about the PAIR system, see http://pair-direct.uspto.gov.

Should you have questions on access to the Private PAIR system, contact the

Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like

assistance from a USPTO Customer Service Representative or access to the

automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-

272-1000.

CKW

ANNE MARIE GRUNBERG
SUPERVISORY PATENT EXAMINER

>ref|NP_569153.1| 🇬 poplyprotein [Citrus yellow mosaic virus]
 gb|AAL18495.1|AF347695_3 🇬 unknown [citrus yellow mosaic virus]
Length=1983

 Score = 736 bits (1900), Expect = 0.0
 Identities = 383/725 (52%), Positives = 505/725 (69%), Gaps = 34/725 (4%)
 Frame = +2

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Query  4145  QVAKSS-VLPRLYSIQAHIHIAPDIVISTTAIIDTGATVCCISEKIVPEAAKEQLNYKVN  4321
             QV K+ V   LY++   + I     + AI+DTGAT CCI  + VP+ A E+ ++ VN
Sbjct  1177  QVTKTRPVKNMLYNMDVRMEIPGIPAFTVKAILDTGATTCCIDSRSVPKDALEENSFVVN  1236

Query  4322  isgissqqqiqHRLKRGTLEIASNKYALPLCYIIELNDKDDFSMILGCNFFKHMGGGMRF  4501
             SGI+S+QQ++ +LK G + I  + ++P CY  E+   D  +ILGCNF + M GG+R
Sbjct  1237  FSGINSKQQVKQKLKTGKMFINEHYFRIPYCYSFEMQIGDGIQLILGCNFIRSMYGGVRL  1296

Query  4502  EGPHVTFYKGITTLSTSYANTGIDTEHEQ------------------ITSTTSQSFKER  4624
             EG +TFYK IT+++T A + E E+                T     F+++
Sbjct  1297  EGNTITFYKQITSINTRLAAPLLKQEEEEKEEELNLEEHRLIQEMVAYSTERPFVQFQQK  1356

Query  4625  FSPLMNELKAAGYIGEDPLKHWSKNKVTCKLDLKNTEITIQDKPLRHITPALEQSYGRHV  4804
             F+ L+ +LKA GYIGE+P+K+W+KN+V C LD+KN ++ I+D+PL+H+TP +E+S+ +HV
Sbjct  1357  FAGLIQDLKAQGYIGEEPMKYWAKNQVVCHLDIKNPDMVIEDRPLKHVTPQMEESFRKHV  1416

Query  4805  NALLMLKVIQPSKSRHRTMAFLVNSGTTVTA-DGKEIKGKERMVFNYKALNDNTYKDQYS  4981
             ALL + I+PSKSRHRT A +VNSGT++      GKE+KGKERMVFNYK LND T KDQYS
Sbjct  1417  EALLKIGAIRPSKSRHRTTAIIVNSGTSIDPITGKEVKGKERMVFNYKRLNDLTNKDQYS  1476

Query  4982  LPNIQLILKKVINSTIYSKFDLKSGFHQVAMDPDSVEWTAFLVPQGLYEWLAMPFGLKNA  5161
             LP IQ IL+++  STI+SKFDLKSGFHQVAM PDS+EWTAF VP GLYEWL MPFGLKNA
Sbjct  1477  LPGIQTILQRLKGSTIFSKFDLKSGFHQVAMHPDSIEWTAFWVPSGLYEWLVMPFGLKNA  1536

Query  5162  PAVFQRKMDAVFKGCEKFLAVYIDDILVFSNNEEDHAKHLVIMLQRCKEHGLVLSPTKMN  5341
             PA+FQRKMD  FKG E F+AVYIDDILVFS  E+DH KHL IML  C+++GL+LSPTKM
Sbjct  1537  PAIFQRKMDHCFKGTEAFIAVYIDDILVFSKTEQDHEKHLQIMLAICQKNGLILSPTKMK  1596

Query  5342  IAVREVNFLGATIGSRKVKLQENIIKKILDFDTEKLQSKKGLRSFLGILNYARNHIPNLG  5521
             IA  E+ FLGA I    +KLQ +I++K+L F  ++L+  KGLRS+LG+LNYAR++IP++G
Sbjct  1597  IAQAEIEFLGAIIHKGLIKLQPHIVQKLLTFTNKQLEEVKGLRSWLGLLNYARSYIPHMG  1656

Query  5522  KIAGPLYSKTSIYGDIRFSASDWKLINEIKAIVEKLPPLDYPPEQAYIIIESDGCMEGWG  5701
             ++  PLY+K S  G+ R +  DW LI++I+A V+ LP L+ PP   +IIIE+DGCM+GWG
Sbjct  1657  RLLSPLYAKVSPTGERRMNRQDWALIDKIRAQVQNLPALELPPADCFIIIETDGCMDGWG  1716

Query  5702  AICKWKLAEYDPKSSEQICAYASGKFSPIKSTIDAEITAAMEGLEAFKIHYLDKQKITLR  5881
             +CKWK+A+YDP+SSE++CAYASGKF P KSTIDAEI A M  L  FKI+YLDK + LR
Sbjct  1717  GVCKWKVAQYDPRSSERVCAYASGKFNPPKSTIDAEIHAVMNSLNNFKIYYLDKSSLCLR  1776

Query  5882  TDCQAIISFCNKTSVNKPSRVRWLKFIDYITNTGIDVKFEHIDAKNNVLADTLSRLVNTL  6061
             TDCQAIISF NK++VNKPSRVRW+ F D++T  GI V  EHID KNN LAD LSRLV
Sbjct  1777  TDCQAIISFFNKSNVNKPSRVRWIAFTDFLTGLGIPVNIEHIDGKNNHLADALSRLVTGF  1836

Query  6062  QDL-PWLDEPHQDQTVSL---MQEIEDAP-------LEIKQRSLTCLQRLICRSFMEDST  6208
              P  + QD  L  +QE ++AP        + + RS + R +C FM DS+
Sbjct  1837  VFAEPQCQDKFQDDLGKLEAALQEKKEAPQAMHVEYVSLLIRSADRITRSLC--FMRDSS  1894

Query  6209  EEAIH  6223
             I+
Sbjct  1895  HSRIY  1899
```

 Score = 360 bits (924), Expect = 7e-97
 Identities = 226/608 (37%), Positives = 324/608 (53%), Gaps = 59/608 (9%)
 Frame = +2

```
Query  2069  DLDYPTLISMEK-----------QLVQSSVTSAYNPPTEPLMGQVVYPPA-SAPRPQAET  2212
             + DYP    ++          + V SS S+Y PPT+ M V YPPA +   P
Sbjct  581   EFDYPAFARLQAHEESGRPKPKTEKVLSSAISSYTPPTDTAMTPVAYPPAQNIASPSYNP  640

Query  2213  SSTSERFKNFRAKPYSTPT-----IFLPPAYNQQGAILVLPDDIGLYEDTISRWESITLN  2377
             S    F+ +  K  +        I LP A   GA+ ++P IGL+ +  + WE+IT
Sbjct  641   SPQMPMFEGYYPKRPNFKRDNHAFISLPSAQQNTGALFIMPQQIGLFHEVFTSWEAITKA  700
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Query  2378  MMNEKVWPSNEAKAKYMENLLGEMEKKTWIQWRTTYVSEYDALVQQSDE---TQNLLSQV  2548
             + ++      KA+++EN+LG EK W QWR Y EY+ LV +D    TQN+LSQ+
Sbjct  701   YVAQQGITDPRDKAEFIENMLGPTEKIIWTQWRMGYADEYENLVTTADGREGTQNILSQM  760

Query  2549  RRIFLLQDPYQGSTAEQDQAYNDLERISCDNIKDLIPYLIQFRNLAAKSGRLFLGPELSE  2728
             RR+F L+DP GSTA QD+AY DLER++CD++K ++ YL F +AAK+GR+F+GPELSE
Sbjct  761   RRVFSLEDPTTGSTAVQDEAYRDLERLTCDSVKHIVQYLNDFMRIAAKTGRMFIGPELSE  820

Query  2729  KLFRKMPPLIGKEIETAFIAKHGNANITVMPRIHFAYHYLAELCKKAALQRSLKDLSFCN  2908
             KL+ KMP +G+ ++ A+ KH   + V PRI FAY YL  CK AA +RSLK+LSFC+
Sbjct  821   KLWLKMPGDLGQRMKKAYEEKHPGNIVGVCPRILFAYKYLEGECKDAAFRRSLKNLSFCS  880

Query  2909  QIPLPGIY--TKGNKKFGLRKARTYKGKPHPTHVRVFKKAKYQRTKKCKCFICGEPGHFA  3082
              IP+PG Y   G K++G+R+  TYKGKPH TH R+ +K K+ R KKCKC++CGE GHFA
Sbjct  881   SIPIPGYYGGKSGEKRYGVRRTTTYKGKPHSTHARI-EKTKHLRNKKCKCYLCGEEGHFA  939

Query  3083  RECTKQRGNIVRATVHQELAIPDNFdvvsvdadesdssGIYSYSE-NEAPLQEVNSFIHD  3259
            ·REC   R N+ R + + L +PD+ ++VS+D + DS  I+S SE  EA  E   F+
Sbjct  940   RECPNDRRNVKRVAMFEGLDLPDDCEIVSIDEGDPDSDAIFSISEGEEAGTLEEQCFVFQ  999

Query  3260  ENIFFLSDADEFESPQQHLHETVNMLQSRSAYLPQVAVGEEKLNCSHIWLQDVDIPSDKH  3439
             E                   L R Y  V + +E  C HW ++ I   H
Sbjct  1000  EEC----------------NGTYWLGKRGGYQDLVQISKEIYYCQHEWEENQPINDPAH  1042·

Query  3440  -KCHTCRRDTQKHYRLECQKCKFLVCSLCTIPYLG--ITMQFRQKQKSQPENPNLVRELL  3610
              +C+ C+R+T + RL C+ C   C +C Y    IT+Q      P+ P  + LL
Sbjct  1043  VRCYPCKRETTQRARLHCKLCHITSCLMCGPTYFNKKITVQ------PMPQAPFNQKGLL  1096

Query  3611  EHAIFLEEKCKNQ--ELLSETQIERIVSSEKQVKFYGILPTKKSNKS-AGYDLQSNID--  3775
             +       C N+   L E  + ++ E++++    L ++S K AG D +   D
Sbjct  1097  QQQQEYIAWCNNEIARLKEEVAFYKQLAQERELQ----LQLEQSRKELAGVDSRRRKDKG  1152

Query  3776  IEIPPGKC  3799
             I I  G C
Sbjct  1153  IVIDEGSC  1160

 Score =  261 bits (668),  Expect = 3e-67
 Identities = 138/327 (42%),  Positives = 200/327 (61%),  Gaps = 18/327 (5%)
 Frame = +2

Query  911   PSTSSTV------PSQQDQIRDYRNMQRVRHTAERAARRIFPGRFNRTLESQINPEAEIR  1072
             P+T++ V      P  DQIRDYR  QR RH  R   ++   +N+TLE  ++PE  ++
Sbjct  15    PATTARVEERDNTPLYDDQIRDYRQWQRRRHNMGRRWNQLIGRPYNQTLEQVVDPEVALQ  74

Query  1073  LSQQRRAAMVPAEVLYNTSPSTRNQKVYQHYSEERILCTGQNQQLNLPFINESSYRALRE  1252
             LS Q RA +VPAEVLY + +    R+ +VY H SEE ILC  Q++  I   S   L
Sbjct  75    LSMQERARLVPAEVLYRSRTDDRHHQVYIHKSEEAILCV-DGDQVDRLLIQPESAEQLSR  133

Query  1253  SGQQHLHIGLIMIRVHPLHRRNAGTTALIVPRDIRWNDDRSIIGTMEIDLSAGSQIVYIA  1432
             SG  +H+G++ +R+  LHR++ GTTAL+V RD RW  D+SI  TME+DL+ G Q+VYI
Sbjct  134   SGMSFIHMGIVQVRIQILHRQHEGTTALVVFRDNRWQGDQSIFATMELDLTKGMQMVYII  193

Query  1433  PNIMLSVEDFYRNIQLAIQTQGYENWNSAESNLLISRALIGRLTNDSFTGFQYNISNVAE  1612
             P+ M++V DF RN+Q++I T+GY NW + E+NLL++R ++GRL+N     F Y I NV +
Sbjct  194   PDTMMTVRDFCRNVQISILTKGYGNWQNGEANLLVTRGIVGRLSNTPNVAFAYQIQNVTD  253

Query  1613  YLHSHGVQAIEGQAHPRT--LGNRWILQ-APAPPRSLVPQNVETTTLLDGNVSIRFSNYH  1783
             YL SHG+QA+ G+ +      G +W L+ + P  + P NV+T  ++DG++S+RF++Y
Sbjct  254   YLVSHGIQALPGRRYSTADIQGQQWFLRPSNIPAVPMAPTNVDTRNMIDGSISLRFNSYQ  313

Query  1784  QAP------VNDTQDNSHPDIQEDENQ  1846
              AP         N   +  PD EDE Q
Sbjct  314   PAPDPTPVAYNQHDEEVPPD--EDEEQ  338
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